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1600

RAW SEQUENCE LISTING

DATE: 12/19/2003

PATENT APPLICATION: US/09/831,050A

TIME: 10:37:16

Input Set : N:\AMC\I831050A.raw

Output Set: N:\CRF4\12182003\I831050A.raw

ENTERED

1 <110> APPLICANT: SHONE, Clifford Charles
 2 SUTTON, John Mark
 3 HALLIS, Bassam
 4 SILMAN, Nigel
 5 <120> TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
 6 <130> FILE REFERENCE: 1581.0800000
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/831,050A
 8 <141> CURRENT FILING DATE: 2001-08-20
 9 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03699
 10 <151> PRIOR FILING DATE: 1998-11-05
 11 <160> NUMBER OF SEQ ID NOS: 14
 12 <170> SOFTWARE: PatentIn Ver. 2.1
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 204
 16 <212> TYPE: PRT
 17 <213> ORGANISM: Bacillus caldotenax
 18 <400> SEQUENCE: 1
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 20 1 5 10 15
 21 Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
 22 20 25 30
 23 Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
 24 35 40 45
 25 Leu Gln Asn Lys Ser Leu Glu Leu Leu Ser Asn Leu Glu Ala Leu
 26 50 55 60
 27 Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
 28 65 70 75 80
 29 Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
 30 85 90 95
 31 Pro Thr Gly Glu Leu Ala Glu Ala Ile Asn Lys Lys Phe Gly Ser Phe
 32 100 105 110
 33 Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
 34 115 120 125
 35 Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
 36 130 135 140
 37 Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
 38 145 150 155 160
 39 Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
 40 165 170 175
 41 Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Ile Val Asn Trp Asp
 42 180 185 190
 43 Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys
 44 195 200

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46 <210> SEQ ID NO: 2
47 <211> LENGTH: 204
48 <212> TYPE: PRT
49 <213> ORGANISM: Bacillus stearothermophilus
50 <400> SEQUENCE: 2
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52       1             5             10             15
53   Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
54               20             25             30
55   Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
56       35             40             45
57   Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
58       50             55             60
59   Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
60       65             70             75             80
61   Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
62               85             90             95
63   Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
64       100            105            110
65   Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
66       115            120            125
67   Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
68       130            135            140
69   Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
70       145            150            155            160
71   Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
72               165            170            175
73   Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp
74       180            185            190
75   Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys
76       195            200

78 <210> SEQ ID NO: 3
79 <211> LENGTH: 1067
80 <212> TYPE: PRT
81 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Description of Artificial Sequence:construct
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85   Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu
86       1             5             10             15
87   Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
88               20             25             30
89   Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
90       35             40             45
91   Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
92       50             55             60
93   Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
94       65             70             75             80
95   Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu

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96					85					90					95	
97	Pro	Thr	Gly	Glu	Leu	Ala	Asp	Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe
98					100					105				110		
99	Thr	Ala	Phe	Lys	Asp	Glu	Phe	Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly
100					115					120				125		
101	Ser	Gly	Trp	Ala	Trp	Leu	Val	Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr
102					130					135				140		
103	Ser	Thr	Pro	Asn	Gln	Asp	Ser	Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile
104					145					150				155		160
105	Leu	Gly	Leu	Asp	Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn
106					165					170				175		
107	Arg	Arg	Pro	Glu	Tyr	Ile	Ala	Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp
108					180					185				190		
109	Glu	Val	Ala	Lys	Arg	Tyr	Ser	Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys
110					195					200				205		
111	Gly	Leu	Val	Pro	Arg	Gly	Ser	Gly	Pro	Gly	Ser	Ala	Leu	Asn	Asp	Leu
112					210					215				220		
113	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe	Ser	Pro	Ser	Glu	Asp
114					225					230				235		240
115	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Thr
116					245					250				255		
117	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp	Leu	Ile	Gln	Gln
118					260					265				270		
119	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu	Asn	Ile	Ser	Ile
120					275					280				285		
121	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu	Glu	Leu	Met	Pro	Asn
122					290					295				300		
123	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu	Leu	Asp	Lys	Tyr	Thr
124					305					310				315		320
125	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu	His	Gly	Lys	Ser	Arg
126					325					330				335		
127	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu	Leu	Asn	Pro	Ser	Arg
128					340					345				350		
129	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	Lys	Lys	Val	Asn	Lys	Ala
130					355					360				365		
131	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu	Gln	Leu	Val	Tyr	Asp
132					370					375				380		
133	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr	Asp	Lys	Ile	Ala	Asp
134					385					390				395		400
135	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu	Asn	Ile	Gly	Asn
136					405					410				415		
137	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala	Leu	Ile	Phe	Ser	Gly	Ala
138					420					425				430		
139	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	Ala	Ile	Pro	Val	Leu	Gly
140					435					440				445		
141	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	Lys	Val	Leu	Thr	Val	Gln
142					450					455				460		
143	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	Glu	Lys	Trp	Asp	Glu	Val
144					465					470				475		480

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145 Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile
146                               485                               490                               495
147 Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu
148                               500                               505                               510
149 Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu
150                               515                               520                               525
151 Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu
152                               530                               535                               540
153 Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn
154                               545                               550                               555                               560
155 Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val
156                               565                               570                               575
157 Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys
158                               580                               585                               590
159 Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu
160                               595                               600                               605
161 Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu
162                               610                               615                               620
163 Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr
164                               625                               630                               635                               640
165 Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser
166                               645                               650                               655
167 Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly
168                               660                               665                               670
169 Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe
170                               675                               680                               685
171 Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val
172                               690                               695                               700
173 Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile
174                               705                               710                               715                               720
175 Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile
176                               725                               730                               735
177 Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly
178                               740                               745                               750
179 Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val
180                               755                               760                               765
181 Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
182                               770                               775                               780
183 Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile
184                               785                               790                               795                               800
185 Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly
186                               805                               810                               815
187 Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg
188                               820                               825                               830
189 Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys
190                               835                               840                               845
191 Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn
192                               850                               855                               860
193 Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys

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194      865      870      875      880
195      Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val
196      885      890      895
197      Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly
198      900      905      910
199      Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly
200      915      920      925
201      Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
202      930      935      940
203      Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys
204      945      950      955      960
205      Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile
206      965      970      975
207      Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val
208      980      985      990
209      Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met
210      995      1000      1005
211      Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His
212      1010      1015      1020
213      Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg
214      1025      1030      1035      1040
215      Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile
216      1045      1050      1055
217      Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
218      1060      1065
220 <210> SEQ ID NO: 4
221 <211> LENGTH: 1070
222 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence:construct
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229      Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
230      20      25      30
231      Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
232      35      40      45
233      Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
234      50      55      60
235      Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
236      65      70      75      80
237      Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
238      85      90      95
239      Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
240      100      105      110
241      Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
242      115      120      125
243      Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr

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VERIFICATION SUMMARY

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L:7 M:270 C: Current Application Number differs, Wrong Format